

10/526049

SEQUENCE LISTING

SEQUENCE LISTING

<110> SODE, Koji; ARKRAY, Inc.; UNITIKA LTD.

5

<120> Method for Preparing Glucose Dehydrogenase

<130> WO-AR2003-7

10 <150> JP 2002/253752

<151> 2002-8-30

<160> 5

15 <210> 1

<211> 3706

<212> DNA

<213> Burkholderia cepacia

20 <220>

<221> CDS

<222> (258) .. (761)

<220>

25 <221> CDS

<222> (764) .. (2380)

<220>

<221> CDS

<222> (2386).. (3660)

<400> 1

```
aagctttctg tttgattgca cgcgattcta accgagcgtc tgtgaggcgg aacgcgacat 60
5 gcttcgtgtc gcacacgtgt cgcgccgacg acacaaaaat gcagcgaaat ggctgatcgt 120
tacgaatggc tgacacattg aatggactat aaaaccattg tccgttccgg aatgtgcgcg 180
tacatttcag gtccgcgcgcg atttttgaga aatatcaagc gtggttttcc cgaatccggt 240
gttcgagaga aggaaac atg cac aac gac aac act ccc cac tcg cgt cgc 290

Met His Asn Asp Asn Thr Pro His Ser Arg Arg
10 1 5 10
cac ggc gac gca gcc gca tca ggc atc acg cgg cgt caa tgg ttg caa 338
His Gly Asp Ala Ala Ala Ser Gly Ile Thr Arg Arg Gln Trp Leu Gln
15 15 20 25
ggc gcg ctg gcg ctg acc gca gcg ggc ctc acg ggt tcg ctg aca ttg 386
Gly Ala Leu Ala Leu Thr Ala Ala Gly Leu Thr Gly Ser Leu Thr Leu
20 30 35 40
cgg gcg ctt gca gac aac ccc ggc act gcg ccg ctc gat acg ttc atg 434
Arg Ala Leu Ala Asp Asn Pro Gly Thr Ala Pro Leu Asp Thr Phe Met
45 50 55
acg ctt tcc gaa tcg ctg acc ggc aag aaa ggg ctc agc cgc gtg atc 482
Thr Leu Ser Glu Ser Leu Thr Gly Lys Lys Gly Leu Ser Arg Val Ile
60 65 70 75
ggc gag cgc ctg ctg cag gcg ctg cag aag ggc tcg ttc aag acg gcc 530
Gly Glu Arg Leu Leu Gln Ala Leu Gln Lys Gly Ser Phe Lys Thr Ala
25 80 85 90
gac agc ctg ccg cag ctc gcc ggc gcg ctc gcg tcc ggt tcg ctg acg 578
Asp Ser Leu Pro Gln Leu Ala Gly Ala Leu Ala Ser Gly Ser Leu Thr
95 100 105
cct gaa cag gaa tcg ctc gca ctg acg atc ctc gag gcc tgg tat ctc 626
```


	gtg ggc ggc acg acg tgg cac tgg gcc gcg tcg gcg tgg cgc ttc att	1105
	Val Gly Gly Thr Thr Trp His Trp Ala Ala Ser Ala Trp Arg Phe Ile	
	270 275 280	
	ccg aac gac ttc aag atg aag agc gtg tac ggc gtc ggc cgc gac tgg	1153
5	Pro Asn Asp Phe Lys Met Lys Ser Val Tyr Gly Val Gly Arg Asp Trp	
	285 290 295	
	ccg atc cag tac gac gat ctc gag ccg tac tat cag cgc gcg gag gaa	1201
	Pro Ile Gln Tyr Asp Asp Leu Glu Pro Tyr Tyr Gln Arg Ala Glu Glu	
	300 305 310	
10	gag ctc ggc gtg tgg ggc ccg ggc ccc gag gaa gat ctg tac tcg ccg	1249
	Glu Leu Gly Val Trp Gly Pro Gly Pro Glu Glu Asp Leu Tyr Ser Pro	
	315 320 325 330	
	cgc aag cag ccg tat ccg atg ccg ccg ctg ccg ttg tcg ttc aac gag	1297
	Arg Lys Gln Pro Tyr Pro Met Pro Pro Leu Pro Leu Ser Phe Asn Glu	
15	335 340 345	
	cag acc atc aag acg gcg ctg aac aac tac gat ccg aag ttc cat gtc	1345
	Gln Thr Ile Lys Thr Ala Leu Asn Asn Tyr Asp Pro Lys Phe His Val	
	350 355 360	
	gtg acc gag ccg gtc gcg cgc aac agc cgc ccg tac gac ggc cgc ccg	1393
20	Val Thr Glu Pro Val Ala Arg Asn Ser Arg Pro Tyr Asp Gly Arg Pro	
	365 370 375	
	act tgt tgc ggc aac aac aac tgc atg ccg atc tgc ccg atc ggc gcg	1441
	Thr Cys Cys Gly Asn Asn Asn Cys Met Pro Ile Cys Pro Ile Gly Ala	
	380 385 390	
25	atg tac aac ggc atc gtg cac gtc gag aag gcc gaa cgc gcc ggc gcg	1489
	Met Tyr Asn Gly Ile Val His Val Glu Lys Ala Glu Arg Ala Gly Ala	
	395 400 405 410	
	aag ctg atc gag aac gcg gtc gtc tac aag ctc gag acg ggc ccg gac	1537
	Lys Leu Ile Glu Asn Ala Val Val Tyr Lys Leu Glu Thr Gly Pro Asp	

	415	420	425	
	aag cgc atc gtc gcg gcg ctc tac aag gac aag acg ggc gcc gag cat			1585
	Lys Arg Ile Val Ala Ala Leu Tyr Lys Asp Lys Thr Gly Ala Glu His			
	430	435	440	
5	cgc gtc gaa ggc aag tat ttc gtg ctc gcc gcg aac ggc atc gag acg			1633
	Arg Val Glu Gly Lys Tyr Phe Val Leu Ala Ala Asn Gly Ile Glu Thr			
	445	450	455	
	ccg aag atc ctg ctg atg tcc gcg aac cgc gat ttc ccg aac ggt gtc			1681
	Pro Lys Ile Leu Leu Met Ser Ala Asn Arg Asp Phe Pro Asn Gly Val			
10	460	465	470	
	gcg aac agc tcg gac atg gtc ggc cgc aac ctg atg gac cat ccg ggc			1729
	Ala Asn Ser Ser Asp Met Val Gly Arg Asn Leu Met Asp His Pro Gly			
	475	480	485	490
	acc ggc gtg tcg ttc tat gcg agc gag aag ctg tgg ccg ggc cgc ggc			1777
15	Thr Gly Val Ser Phe Tyr Ala Ser Glu Lys Leu Trp Pro Gly Arg Gly			
	495	500	505	
	ccg cag gag atg acg tcg ctg atc ggt ttc cgc gac ggt ccg ttc cgc			1825
	Pro Gln Glu Met Thr Ser Leu Ile Gly Phe Arg Asp Gly Pro Phe Arg			
	510	515	520	
20	gcg acc gaa gcg gcg aag aag atc cac ctg tcg aac ctg tcg cgc atc			1873
	Ala Thr Glu Ala Ala Lys Lys Ile His Leu Ser Asn Leu Ser Arg Ile			
	525	530	535	
	gac cag gag acg cag aag atc ttc aag gcc ggc aag ctg atg aag ccc			1921
	Asp Gln Glu Thr Gln Lys Ile Phe Lys Ala Gly Lys Leu Met Lys Pro			
25	540	545	550	
	gac gag ctc gac gcg cag atc cgc gac cgt tcc gca cgc tac gtg cag			1969
	Asp Glu Leu Asp Ala Gln Ile Arg Asp Arg Ser Ala Arg Tyr Val Gln			
	555	560	565	570
	ttc gac tgc ttc cac gaa atc ctg ccg caa ccc gag aac cgc atc gtg			2017

	Phe Asp Cys Phe His Glu Ile Leu Pro Gln Pro Glu Asn Arg Ile Val	
	575	580 585
	ccg agc aag acg gcg acc gat gcg atc ggc att ccg cgc ccc gag atc	2065
	Pro Ser Lys Thr Ala Thr Asp Ala Ile Gly Ile Pro Arg Pro Glu Ile	
5	590	595 600
	acg tat gcg atc gac gac tac gtg aag cgc ggc gcc gcg cat acg cgc	2113
	Thr Tyr Ala Ile Asp Asp Tyr Val Lys Arg Gly Ala Ala His Thr Arg	
	605	610 615
	gag gtc tac gcg acc gcc gcg aag gtg ctc ggc ggc acg gac gtc gtg	2161
10	Glu Val Tyr Ala Thr Ala Ala Lys Val Leu Gly Gly Thr Asp Val Val	
	620	625 630
	ttc aac gac gaa ttc gcg ccg aac aat cac atc acg ggc tcg acg atc	2209
	Phe Asn Asp Glu Phe Ala Pro Asn Asn His Ile Thr Gly Ser Thr Ile	
	635	640 645 650
15	atg ggc gcc gat gcg cgc gac tcc gtc gtc gac aag gac tgc cgc acg	2257
	Met Gly Ala Asp Ala Arg Asp Ser Val Val Asp Lys Asp Cys Arg Thr	
	655	660 665
	ttc gac cat ccg aac ctg ttc att tcg agc agc gcg acg atg ccg acc	2305
	Phe Asp His Pro Asn Leu Phe Ile Ser Ser Ser Ala Thr Met Pro Thr	
20	670	675 680
	gtc ggt acc gta aac gtg acg ctg acg atc gcc gcg ctc gcg ctg cgg	2353
	Val Gly Thr Val Asn Val Thr Leu Thr Ile Ala Ala Leu Ala Leu Arg	
	685	690 695
	atg tcg gac acg ctg aag aag gaa gtc tgacc gtg cgg aaa tct act ctc	2403
25	Met Ser Asp Thr Leu Lys Lys Glu Val	Val Arg Lys Ser Thr Leu
	700	705 710
	act ttc ctc atc gcc ggc tgc ctc gcg ttg ccg ggc ttc gcg cgc gcg	2451
	Thr Phe Leu Ile Ala Gly Cys Leu Ala Leu Pro Gly Phe Ala Arg Ala	
	715	720 725

	gcc gat gcg gcc gat ccg gcg ctg gtc aag cgc ggc gaa tac ctc gcg	2499
	Ala Asp Ala Ala Asp Pro Ala Leu Val Lys Arg Gly Glu Tyr Leu Ala	
	730 735 740 745	
	acc gcc atg ccg gta ccg atg ctc ggc aag atc tac acg agc aac atc	2547
5	Thr Ala Met Pro Val Pro Met Leu Gly Lys Ile Tyr Thr Ser Asn Ile	
	750 755 760	
	acg ccc gat ccc gat acg ggc gac tgc atg gcc tgc cac acc gtg aag	2595
	Thr Pro Asp Pro Asp Thr Gly Asp Cys Met Ala Cys His Thr Val Lys	
	765 770 775	
10	ggc ggc aag ccg tac gcg ggc ggc ctt ggc ggc atc ggc aaa tgg acg	2643
	Gly Gly Lys Pro Tyr Ala Gly Gly Leu Gly Gly Ile Gly Lys Trp Thr	
	780 785 790	
	ttc gag gac ttc gag cgc gcg gtg cgg cac ggc gtg tcg aag aac ggc	2691
	Phe Glu Asp Phe Glu Arg Ala Val Arg His Gly Val Ser Lys Asn Gly	
15	795 800 805	
	gac aac ctg tat ccg gcg atg ccg tac gtg tcg tac gcg aag atc aag	2739
	Asp Asn Leu Tyr Pro Ala Met Pro Tyr Val Ser Tyr Ala Lys Ile Lys	
	810 815 820 825	
	gac gac gac gta cgc gcg ctg tac gcc tac ttc atg cac ggc gtc gag	2787
20	Asp Asp Asp Val Arg Ala Leu Tyr Ala Tyr Phe Met His Gly Val Glu	
	830 835 840	
	ccg gtc aag cag gcg ccg ccg aag aac gag atc cca gcg ctg cta agc	2835
	Pro Val Lys Gln Ala Pro Pro Lys Asn Glu Ile Pro Ala Leu Leu Ser	
	845 850 855	
25	atg cgc tgg ccg ctg aag atc tgg aac tgg ctg ttc ctg aag gac ggc	2883
	Met Arg Trp Pro Leu Lys Ile Trp Asn Trp Leu Phe Leu Lys Asp Gly	
	860 865 870	
	ccg tac cag ccg aag ccg tcg cag agc gcc gaa tgg aat cgc ggc gcg	2931
	Pro Tyr Gln Pro Lys Pro Ser Gln Ser Ala Glu Trp Asn Arg Gly Ala	

	875	880	885	
	tat ctg gtg cag ggt ctc gcg cac tgc agc acg tgc cac acg ccg cgc			2979
	Tyr Leu Val Gln Gly Leu Ala His Cys Ser Thr Cys His Thr Pro Arg			
	890	895	900	905
5	ggc atc gcg atg cag gag aag tcg ctc gac gaa acc ggc ggc agc ttc			3027
	Gly Ile Ala Met Gln Glu Lys Ser Leu Asp Glu Thr Gly Gly Ser Phe			
		910	915	920
	ctc gcg ggg tcg gtg ctc gcc ggc tgg gac ggc tac aac atc acg tcg			3075
	Leu Ala Gly Ser Val Leu Ala Gly Trp Asp Gly Tyr Asn Ile Thr Ser			
10		925	930	935
	gac ccg aat gcg ggg atc ggc agc tgg acg cag cag cag ctc gtg cag			3123
	Asp Pro Asn Ala Gly Ile Gly Ser Trp Thr Gln Gln Gln Leu Val Gln			
		940	945	950
	tat ttg cgc acc ggc agc gtg ccg ggc gtc gcg cag gcg gcc ggg ccg			3171
15	Tyr Leu Arg Thr Gly Ser Val Pro Gly Val Ala Gln Ala Ala Gly Pro			
		955	960	965
	atg gcc gag gcg gtc gag cac agc ttc tcg aag atg acc gaa gcg gac			3219
	Met Ala Glu Ala Val Glu His Ser Phe Ser Lys Met Thr Glu Ala Asp			
		970	975	980
				985
20	atc ggt gcg atc gcc acg tac gtc cgc acg gtg ccg gcc gtt gcc gac			3267
	Ile Gly Ala Ile Ala Thr Tyr Val Arg Thr Val Pro Ala Val Ala Asp			
		990	995	1000
	agc aac gcg aag cag ccg cgg tcg tcg tgg ggc aag ccg gcc gag gac			3315
	Ser Asn Ala Lys Gln Pro Arg Ser Ser Trp Gly Lys Pro Ala Glu Asp			
25		1005	1010	1015
	ggg ctg aag ctg cgc ggt gtc gcg ctc gcg tcg tcg ggc atc gat ccg			3363
	Gly Leu Lys Leu Arg Gly Val Ala Leu Ala Ser Ser Gly Ile Asp Pro			
		1020	1025	1030
	gcg cgg ctg tat ctc ggc aac tgc gcg acg tgc cac cag atg cag ggc			3411

	Ala Arg Leu Tyr Leu Gly Asn Cys Ala Thr Cys His Gln Met Gln Gly	
	1035 1040 1045	
	aag ggc acg ccg gac ggc tat tac ccg tcg ctg ttc cac aac tcc acc	3459
	Lys Gly Thr Pro Asp Gly Tyr Tyr Pro Ser Leu Phe His Asn Ser Thr	
5	1050 1055 1060 1065	
	gtc ggc gcg tcg aat ccg tcg aac ctc gtg cag gtg atc ctg aac ggc	3507
	Val Gly Ala Ser Asn Pro Ser Asn Leu Val Gln Val Ile Leu Asn Gly	
	1070 1075 1080	
	gtg cag cgc aag atc ggc agc gag gat atc ggg atg ccc gct ttc cgc	3555
10	Val Gln Arg Lys Ile Gly Ser Glu Asp Ile Gly Met Pro Ala Phe Arg	
	1085 1090 1095	
	tac gat ctg aac gac gcg cag atc gcc gcg ctg acg aac tac gtg acc	3603
	Tyr Asp Leu Asn Asp Ala Gln Ile Ala Ala Leu Thr Asn Tyr Val Thr	
	1100 1105 1110	
15	gcg cag ttc ggc aat ccg gcg gcg aag gtg acg gag cag gac gtc gcg	3651
	Ala Gln Phe Gly Asn Pro Ala Ala Lys Val Thr Glu Gln Asp Val Ala	
	1115 1120 1125	
	aag ctg cgc tga catagtcggg cgcgccgaca cggcgcaacc gataggacag gag	3706
	Lys Leu Arg	
20	1130	

<210> 2
 <211> 168
 <212> PRT
 25 <213> Pseudomonas putida

<400> 2
 Met His Asn Asp Asn Thr Pro His Ser Arg Arg His Gly Asp Ala Ala
 1 5 10 15

Ala Ser Gly Ile Thr Arg Arg Gln Trp Leu Gln Gly Ala Leu Ala Leu
 20 25 30
 Thr Ala Ala Gly Leu Thr Gly Ser Leu Thr Leu Arg Ala Leu Ala Asp
 35 40 45
 5 Asn Pro Gly Thr Ala Pro Leu Asp Thr Phe Met Thr Leu Ser Glu Ser
 50 55 60
 Leu Thr Gly Lys Lys Gly Leu Ser Arg Val Ile Gly Glu Arg Leu Leu
 65 70 75 80
 Gln Ala Leu Gln Lys Gly Ser Phe Lys Thr Ala Asp Ser Leu Pro Gln
 10 85 90 95
 Leu Ala Gly Ala Leu Ala Ser Gly Ser Leu Thr Pro Glu Gln Glu Ser
 100 105 110
 Leu Ala Leu Thr Ile Leu Glu Ala Trp Tyr Leu Gly Ile Val Asp Asn
 115 120 125
 15 Val Val Ile Thr Tyr Glu Glu Ala Leu Met Phe Gly Val Val Ser Asp
 130 135 140
 Thr Leu Val Ile Arg Ser Tyr Cys Pro Asn Lys Pro Gly Phe Trp Ala
 145 150 155 160
 Asp Lys Pro Ile Glu Arg Gln Ala
 20 165
 <210> 3
 <211> 539
 <212> PRT
 <213> Pseudomonas putida
 25
 <400> 3
 Met Ala Asp Thr Asp Thr Gln Lys Ala Asp Val Val Val Val Gly Ser
 1 5 10 15
 Gly Val Ala Gly Ala Ile Val Ala His Gln Leu Ala Met Ala Gly Lys

	20	25	30
	Ala Val Ile Leu Leu Glu Ala Gly Pro Arg Met Pro Arg Trp Glu Ile		
	35	40	45
	Val Glu Arg Phe Arg Asn Gln Pro Asp Lys Met Asp Phe Met Ala Pro		
5	50	55	60
	Tyr Pro Ser Ser Pro Trp Ala Pro His Pro Glu Tyr Gly Pro Pro Asn		
	65	70	75
	Asp Tyr Leu Ile Leu Lys Gly Glu His Lys Phe Asn Ser Gln Tyr Ile		
	85	90	95
10	Arg Ala Val Gly Gly Thr Thr Trp His Trp Ala Ala Ser Ala Trp Arg		
	100	105	110
	Phe Ile Pro Asn Asp Phe Lys Met Lys Ser Val Tyr Gly Val Gly Arg		
	115	120	125
	Asp Trp Pro Ile Gln Tyr Asp Asp Leu Glu Pro Tyr Tyr Gln Arg Ala		
15	130	135	140
	Glu Glu Glu Leu Gly Val Trp Gly Pro Gly Pro Glu Glu Asp Leu Tyr		
	145	150	155
	Ser Pro Arg Lys Gln Pro Tyr Pro Met Pro Pro Leu Pro Leu Ser Phe		
	165	170	175
20	Asn Glu Gln Thr Ile Lys Thr Ala Leu Asn Asn Tyr Asp Pro Lys Phe		
	180	185	190
	His Val Val Thr Glu Pro Val Ala Arg Asn Ser Arg Pro Tyr Asp Gly		
	195	200	205
	Arg Pro Thr Cys Cys Gly Asn Asn Asn Cys Met Pro Ile Cys Pro Ile		
25	210	215	220
	Gly Ala Met Tyr Asn Gly Ile Val His Val Glu Lys Ala Glu Arg Ala		
	225	230	235
	Gly Ala Lys Leu Ile Glu Asn Ala Val Val Tyr Lys Leu Glu Thr Gly		
	245	250	255

	Pro	Asp	Lys	Arg	Ile	Val	Ala	Ala	Leu	Tyr	Lys	Asp	Lys	Thr	Gly	Ala	
						260					265					270	
	Glu	His	Arg	Val	Glu	Gly	Lys	Tyr	Phe	Val	Leu	Ala	Ala	Asn	Gly	Ile	
					275					280					285		
5	Glu	Thr	Pro	Lys	Ile	Leu	Leu	Met	Ser	Ala	Asn	Arg	Asp	Phe	Pro	Asn	
					290					295					300		
	Gly	Val	Ala	Asn	Ser	Ser	Asp	Met	Val	Gly	Arg	Asn	Leu	Met	Asp	His	
	305					310					315				320		
	Pro	Gly	Thr	Gly	Val	Ser	Phe	Tyr	Ala	Ser	Glu	Lys	Leu	Trp	Pro	Gly	
10					325					330					335		
	Arg	Gly	Pro	Gln	Glu	Met	Thr	Ser	Leu	Ile	Gly	Phe	Arg	Asp	Gly	Pro	
					340					345					350		
	Phe	Arg	Ala	Thr	Glu	Ala	Ala	Lys	Lys	Ile	His	Leu	Ser	Asn	Leu	Ser	
					355					360					365		
15	Arg	Ile	Asp	Gln	Glu	Thr	Gln	Lys	Ile	Phe	Lys	Ala	Gly	Lys	Leu	Met	
	370					375							380				
	Lys	Pro	Asp	Glu	Leu	Asp	Ala	Gln	Ile	Arg	Asp	Arg	Ser	Ala	Arg	Tyr	
	385					390						395			400		
	Val	Gln	Phe	Asp	Cys	Phe	His	Glu	Ile	Leu	Pro	Gln	Pro	Glu	Asn	Arg	
20					405					410					415		
	Ile	Val	Pro	Ser	Lys	Thr	Ala	Thr	Asp	Ala	Ile	Gly	Ile	Pro	Arg	Pro	
					420					425					430		
	Glu	Ile	Thr	Tyr	Ala	Ile	Asp	Asp	Tyr	Val	Lys	Arg	Gly	Ala	Ala	His	
					435					440					445		
25	Thr	Arg	Glu	Val	Tyr	Ala	Thr	Ala	Ala	Lys	Val	Leu	Gly	Gly	Thr	Asp	
	450					455							460				
	Val	Val	Phe	Asn	Asp	Glu	Phe	Ala	Pro	Asn	Asn	His	Ile	Thr	Gly	Ser	
	465					470						475			480		
	Thr	Ile	Met	Gly	Ala	Asp	Ala	Arg	Asp	Ser	Val	Val	Asp	Lys	Asp	Cys	

	485	490	495
	Arg Thr Phe Asp His Pro Asn Leu Phe Ile Ser Ser Ser Ala Thr Met		
	500	505	510
	Pro Thr Val Gly Thr Val Asn Val Thr Leu Thr Ile Ala Ala Leu Ala		
5	515	520	525
	Leu Arg Met Ser Asp Thr Leu Lys Lys Glu Val		
	530	535	
	<210> 4		
10	<211> 27		
	<212> PRT		
	<213> Pseudomonas putida		
	<400> 4		
15	Val Arg Lys Ser Thr Leu Thr Phe Leu Ile Ala Gly Cys Leu Ala Leu		
	1	5	10 15
	Pro Gly Phe Ala Arg Ala Ala Asp Ala Ala Asp		
	20	25	
20	<210> 5		
	<211> 425		
	<212> PRT		
	<213> Pseudomonas putida		
25	<400> 5		
	Val Arg Lys Ser Thr Leu Thr Phe Leu Ile Ala Gly Cys Leu Ala Leu Pro Gly Phe		
	1	5	10 15
	Ala Arg Ala Ala Asp Ala Ala Asp Pro Ala Leu Val Lys Arg Gly Glu Tyr Leu Ala		
	20	25	30 35

Thr Ala Met Pro Val Pro Met Leu Gly Lys Ile Tyr Thr Ser Asn Ile Thr Pro Asp
 40 45 50 55
 Pro Asp Thr Gly Asp Cys Met Ala Cys His Thr Val Lys Gly Gly Lys Pro Tyr Ala
 60 65 70 75Gly
 5 Gly Leu Gly Gly Ile Gly Lys Trp Thr Phe Glu Asp Phe Glu Arg Ala Val Arg
 80 85 90
 95
 His Gly Val Ser Lys Asn Gly Asp Asn Leu Tyr Pro Ala Met Pro Tyr Val Ser Tyr
 100 105 110
 10 Ala Lys Ile Lys Asp Asp Asp Val Arg Ala Leu Tyr Ala Tyr Phe Met His Gly Val
 115 120 125 130
 Glu Pro Val Lys Gln Ala Pro Pro Lys Asn Glu Ile Pro Ala Leu Leu Ser Met Arg
 135 140 145 150
 Trp Pro Leu Lys Ile Trp Asn Trp Leu Phe Leu Lys Asp Gly Pro Tyr Gln Pro Lys
 15 155 160 165 170Pro
 Ser Gln Ser Ala Glu Trp Asn Arg Gly Ala Tyr Leu Val Gln Gly Leu Ala His
 175 180 185 190
 Cys Ser Thr Cys His Thr Pro Arg Gly Ile Ala Met Gln Glu Lys Ser Leu Asp Glu
 195 200 205
 20 Thr Gly Gly Ser Phe Leu Ala Gly Ser Val Leu Ala Gly Trp Asp Gly Tyr Asn Ile
 210 215 220 225
 Thr Ser Asp Pro Asn Ala Gly Ile Gly Ser Trp Thr Gln Gln Gln Leu Val Gln
 230 235 240 245
 Tyr Leu Arg Thr Gly Ser Val Pro Gly Val Ala Gln Ala Ala Gly Pro Met Ala Glu
 25 250 255 260 265
 Ala Val Glu His Ser Phe Ser Lys Met Thr Glu Ala Asp Ile Gly Ala Ile Ala Thr
 270 275 280
 Tyr Val Arg Thr Val Pro Ala Val Ala Asp Ser Asn Ala Lys Gln Pro Arg Ser Ser
 285 290 295 300

Trp Gly Lys Pro Ala Glu Asp Gly Leu Lys Leu Arg Gly Val Ala Leu Ala Ser Ser
 305 310 315 320
 Gly Ile Asp Pro Ala Arg Leu Tyr Leu Gly Asn Cys Ala Thr Cys His Gln Met Gln
 325 330 335 340Gly
 5 Lys Gly Thr Pro Asp Gly Tyr Tyr Pro Ser Leu Phe His Asn Ser Thr Val Gly
 345 350 355 360
 Ala Ser Asn Pro Ser Asn Leu Val Gln Val Ile Leu Asn Gly Val Gln Arg Lys Ile
 365 370 375
 Gly Ser Glu Asp Ile Gly Met Pro Ala Phe Arg Tyr Asp Leu Asn Asp Ala Gln Ile
 10 380 385 390 395
 Ala Ala Leu Thr Asn Tyr Val Thr Ala Gln Phe Gly Asn Pro Ala Ala Lys Val Thr
 400 405 410 415
 Glu Gln Asp Val Ala Lys Leu Arg
 420 425

15